

#7

SEQUENCE LISTING

<110> EINAT, Paz

SKALITER, Rami

FEINSTEIN, Elena

<120> SEQUENCES CHARACTERISTIC OF HYPOXIA-REGULATED GENE TRANSCRIPTION

<130> EINAT=4.1C

<150> US 09/383,096

<151> 1999-08-27

<150> US 09/138,109

<151> 1998-08-21

<150> US 60/098,158

<151> 1998-08-27

<150> US 60/132,684

<151> 1999-05-05

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<170> PatentIn version 3.0

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Cys Asn Val Leu Asn Trp Glu Gln Val Gln Arg Leu Asp Gly Ile Leu
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Gly Pro Ser Ala Phe Ile Pro Val Glu Glu Val Leu Arg Glu Gly Ala											
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Arg	Phe	Ala	Pro	Gly	Gly	Val	Gly	Asp	Ser	Gly	Pro	Gly	Glu	Glu	Gln	20	25	30	
Arg	Glu	Ser	Arg	Ala	Arg	Arg	Gly	Pro	Arg	Gly	Pro	Ser	Ala	Phe	Ile	35	40	45	
Pro	Val	Glu	Glu	Val	Leu	Arg	Glu	Gly	Ala	Glu	Ser	Leu	Glu	Gln	His	50	55	60	
Leu	Gly	Leu	Glu	Ala	Leu	Met	Ser	Ser	Gly	Arg	Val	Asp	Asn	Leu	Ala	65	70	75	80
Val	Val	Met	Gly	Leu	His	Pro	Asp	Tyr	Phe	Thr	Ser	Phe	Trp	Xaa	Leu	85	90	95	
His	Tyr	Leu	Leu	Leu	His	Thr	Asp	Gly	Pro	Leu	Ala	Ser	Ser	Trp	Arg	100	105	110	
His	Tyr	Ile	Ala	Ile	Met	Ala	Ala	Ala	Arg	His	Gln	Cys	Ser	Tyr	Leu	115	120	125	
Val	Gly	Ser	His	Met	Ala	Glu	Phe	Leu	Gln	Thr	Gly	Gly	Asp	Pro	Glu	130	135	140	
Trp	Leu	Leu	Gly	Leu	His	Arg	Ala	Pro	Glu	Lys	Leu	Arg	Lys	Leu	Ser	145	150	155	160

Glu Ile Asn Lys Leu Leu Ala His Arg Pro Trp Leu Ile Thr Lys Glu
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 His Ile Gln Ala Leu Leu Lys Thr Gly Glu His Thr Trp Ser Leu Ala
 180 185 190
 Glu Leu Ile Gln Ala Leu Val Leu Leu Thr His Cys His Ser Leu Ser
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 Ser Phe Val Phe Gly Cys Gly Ile Leu Pro Glu Gly Asp Ala Asp Gly
 210 215 220
 Ser Pro Ala Pro Gln Ala Pro Thr Pro Pro Ser Glu Gln Ser Ser Pro
 225 230 235 240
 Pro Ser Arg Asp Pro Leu Asn Asn Ser Gly Gly Phe Glu Ser Ala Arg
 245 250 255
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 Leu Arg Asp Glu Gly Thr Ser Gln Glu Glu Met Glu Ser Arg Phe Glu
 275 280 285
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 290 295 300
 Glu Pro Ser Pro His Pro Asp Met Leu Cys Phe Val Glu Asp Pro Thr
 305 310 315 320
 Phe Gly Tyr Glu Asp Phe Thr Arg Arg Gly Ala Gln Ala Pro Pro Thr
 325 330 335
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 340 345 350
 Gln Arg Leu Tyr Pro Glu Gly Gly Gln Leu Leu Asp Glu Lys Phe Gln
 355 360 365
 Ala Ala Tyr Ser Leu Thr Tyr Asn Thr Ile Ala Met His Ser Gly Val
 370 375 380
 Asp Thr Ser Val Leu Arg Arg Ala Ile Trp Asn Tyr Ile His Cys Val
 385 390 395 400
 Phe Gly Ile Arg Tyr Asp Asp Tyr Asp Tyr Gly Glu Val Asn Gln Leu
 405 410 415
 Leu Glu Arg Asn Leu Lys Val Tyr Ile Lys Thr Val Ala Cys Tyr Pro
 420 425 430
 Glu Lys Thr Thr Arg Arg Met Tyr Asn Leu Phe Trp Arg His Phe Arg
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 His Ser Glu Lys Val His Val Asn Leu Leu Leu Leu Glu Ala Arg Met
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465

470

475

480

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<211> 4138

<212> DNA

<213> Homo sapiens

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<211> 1303

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> "n" at every occurrence is unknown

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<210> 7

<211> 244

<212> PRT

<213> Homo sapiens

<220>

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<223> "Xaa" at position 118 is unknown

<400> 7

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35 40 45
Pro Glu Asn Tyr Val Pro Thr Val Phe Glu Asn Tyr Thr Ala Ser Phe
50 55 60
Glu Ile Asp Thr Gln Arg Ile Glu Leu Ser Leu Trp Asp Thr Ser Gly
65 70 75 80
Ser Pro Tyr Tyr Asp Asn Val Arg Pro Leu Ser Tyr Pro Asp Ser Asp
85 90 95
Ala Val Leu Ile Cys Phe Asp Ile Ser Arg Pro Glu Thr Leu Asp Ser
100 105 110
Val Leu Lys Lys Trp Xaa Gly Glu Ile Gln Glu Phe Cys Pro Asn Thr
115 120 125
Lys Met Leu Leu Val Gly Cys Lys Ser Asp Leu Arg Thr Asp Val Ser
130 135 140
Thr Leu Val Glu Leu Ser Asn His Arg Gln Thr Pro Val Ser Tyr Asp
145 150 155 160
Gln Gly Ala Asn Met Ala Lys Gln Ile Gly Ala Ala Thr Tyr Ile Glu
165 170 175
Cys Ser Ala Leu Gln Ser Glu Asn Ser Val Arg Asp Ile Phe His Val
180 185 190
Ala Thr Leu Ala Cys Val Asn Lys Thr Asn Lys Asn Val Lys Arg Asn
195 200 205
Lys Ser Gln Arg Ala Thr Lys Arg Ile Ser His Met Pro Ser Arg Pro
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<211> 2479

<212> DNA

<213> Rattus rattus

<220>

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<222> (1)..(2274)

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Leu His Pro Trp Asn Pro Cys Leu Gly Ala Asp Ser Glu Lys Pro Ser
20 25 30
agc atc ccc aca gat aaa tta tta gtc ata act gta gca aca aaa gaa 144
Ser Ile Pro Thr Asp Lys Leu Leu Val Ile Thr Val Ala Thr Lys Glu
35 40 45
agt gat gga ttc cat cga ttt atg cag tca gcc aaa tat ttc aat tat 192
Ser Asp Gly Phe His Arg Phe Met Gln Ser Ala Lys Tyr Phe Asn Tyr
50 55 60
act gtg aag gtc ctt ggt caa gga gaa gaa tgg aga ggt ggt gat gga 240
Thr Val Lys Val Leu Gly Gln Gly Glu Glu Trp Arg Gly Gly Asp Gly
65 70 75 80
att aat agt att gga ggg ggc cag aaa gtg aga tta atg aaa gaa gtc 288
Ile Asn Ser Ile Gly Gly Gly Gln Lys Val Arg Leu Met Lys Glu Val
85 90 95
atg gaa cac tat gct gat caa gat gat ctg gtt gtc atg ttt act gaa 336
Met Glu His Tyr Ala Asp Gln Asp Asp Leu Val Val Met Phe Thr Glu
100 105 110
tgc ttt gat gtc ata ttt gct ggt ggt cca gaa gaa gtt cta aaa aaa 384
Cys Phe Asp Val Ile Phe Ala Gly Gly Pro Glu Glu Val Leu Lys Lys
115 120 125
ttc caa aag gca aac cac aaa gtg gtc ttt gca gca gat gga att ttg 432
Phe Gln Lys Ala Asn His Lys Val Val Phe Ala Ala Asp Gly Ile Leu
130 135 140
tgg cca gat aaa aga cta gca gac aag tat cct gtt gtg cac att ggg 480
Trp Pro Asp Lys Arg Leu Ala Asp Lys Tyr Pro Val Val His Ile Gly
145 150 155 160
aaa cgc tat ctg aat tca gga gga ttt att ggc tat gct cca tat gtc 528
Lys Arg Tyr Leu Asn Ser Gly Gly Phe Ile Gly Tyr Ala Pro Tyr Val

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aac	cgt	ata	gtt	caa	caa	tgg	aat	ctc	cag	gat	aat	gat	gat	gat	cag	576			
Asn	Arg	Ile	Val	Gln	Gln	Trp	Asn	Leu	Gln	Asp	Asn	Asp	Asp	Asp	Gln				
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Asn	Ile	Thr	Leu	Asp	His	Lys	Cys	Lys	Ile	Phe	Gln	Thr	Leu	Asn	Gly				
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Ala	Val	Asp	Glu	Val	Val	Leu	Lys	Phe	Glu	Asn	Gly	Lys	Ala	Arg	Ala	240			
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Lys	Asn	Thr	Phe	Tyr	Glu	Thr	Leu	Pro	Val	Ala	Ile	Asn	Gly	Asn	Gly	255			
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Val	Tyr	His	Glu	Lys	Asp	Ile	Lys	Val	Phe	Phe	Asp	Lys	Ala	Lys	His	350			
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Ala	Glu	Ala	Arg	Asn	Met	Gly	Met	Asp	Phe	Cys	Arg	Gln	Asp	Glu	Lys	380			
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385	390	395	400	
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Arg Thr Leu Lys Ile Leu Ile Glu Gln Asn Arg Lys Ile Ile Ala Pro	405	410	415	
ctt gta act cgt cat gga aag ctg tgg tcc aat ttc tgg gga gca ttg				1296
Leu Val Thr Arg His Gly Lys Leu Trp Ser Asn Phe Trp Gly Ala Leu	420	425	430	
agt cct gat gga tac tat gca cga tct gaa gat tat gtg gat att gtt				1344
Ser Pro Asp Gly Tyr Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val	435	440	445	
caa ggg aat aga gta gga gta tgg aat gtc cca tat atg gct aat gtg				1392
Gln Gly Asn Arg Val Gly Val Trp Asn Val Pro Tyr Met Ala Asn Val	450	455	460	
tac tta att aaa gga aag aca ctc cga tca gag atg aat gaa agg aac				1440
Tyr Leu Ile Lys Gly Lys Thr Leu Arg Ser Glu Met Asn Glu Arg Asn	465	470	475	480
tat ttt gtt cgt gat aaa ctg gat cct gat atg gct ctt tgc cga aat				1488
Tyr Phe Val Arg Asp Lys Leu Asp Pro Asp Met Ala Leu Cys Arg Asn	485	490	495	
gct aga gaa atg act tta caa agg gaa aaa gac tcc cct act ccg gaa				1536
Ala Arg Glu Met Thr Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu	500	505	510	
aca ttc caa atg ctc agc ccc cca aag ggt gta ttt atg tac att tct				1584
Thr Phe Gln Met Leu Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser	515	520	525	
aat aga cat gaa ttt gga agg cta tta tcc act gct aat tac aat act				1632
Asn Arg His Glu Phe Gly Arg Leu Leu Ser Thr Ala Asn Tyr Asn Thr	530	535	540	
tcc cat tat aac aat gac ctc tgg cag att ttt gaa aat cct gtg gac				1680
Ser His Tyr Asn Asn Asp Leu Trp Gln Ile Phe Glu Asn Pro Val Asp	545	550	555	560
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Trp Lys Glu Lys Tyr Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu	565	570	575	
aat ata gtt gaa cag ccc tgt cca gat gtc ttt tgg ttc ccc ata ttt				1776
Asn Ile Val Glu Gln Pro Cys Pro Asp Val Phe Trp Phe Pro Ile Phe	580	585	590	
tct gaa aaa gcc tgt gat gaa ttg gta gaa gaa atg gaa cat tac ggc				1824
Ser Glu Lys Ala Cys Asp Glu Leu Val Glu Glu Met Glu His Tyr Gly	595	600	605	
aaa tgg tct ggg gga aaa cat cat gat agc cgt ata tct ggt ggt tat				1872
Lys Trp Ser Gly Gly Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr				

610	615	620	
gaa aat gtc cca act gat gat atc cac atg aag caa gtt gat ctg gag			1920
Glu Asn Val Pro Thr Asp Asp Ile His Met Lys Gln Val Asp Leu Glu			
625	630	635	640
aat gta tgg ctt cat ttt atc cgg gag ttc att gca cca gtt aca ctg			1968
Asn Val Trp Leu His Phe Ile Arg Glu Phe Ile Ala Pro Val Thr Leu			
	645	650	655
aag gtc ttt gca ggc tat tat acg aag gga ttt gca cta ctg aat ttt			2016
Lys Val Phe Ala Gly Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe			
	660	665	670
gta gta aaa tac tcc cct gaa cga cag cgt tct ctt cgt cct cat cat			2064
Val Val Lys Tyr Ser Pro Glu Arg Gln Arg Ser Leu Arg Pro His His			
	675	680	685
gat gct tct aca ttt acc ata aac att gca ctt aat aac gtg gga gaa			2112
Asp Ala Ser Thr Phe Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu			
690	695	700	

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 1 5 10 15
 Leu His Pro Trp Asn Pro Cys Leu Gly Ala Asp Ser Glu Lys Pro Ser
 20 25 30
 Ser Ile Pro Thr Asp Lys Leu Leu Val Ile Thr Val Ala Thr Lys Glu
 35 40 45
 Ser Asp Gly Phe His Arg Phe Met Gln Ser Ala Lys Tyr Phe Asn Tyr
 50 55 60
 Thr Val Lys Val Leu Gly Gln Gly Glu Glu Trp Arg Gly Gly Asp Gly
 65 70 75 80
 Ile Asn Ser Ile Gly Gly Gly Gln Lys Val Arg Leu Met Lys Glu Val
 85 90 95
 Met Glu His Tyr Ala Asp Gln Asp Asp Leu Val Val Met Phe Thr Glu
 100 105 110
 Cys Phe Asp Val Ile Phe Ala Gly Gly Pro Glu Glu Val Leu Lys Lys
 115 120 125
 Phe Gln Lys Ala Asn His Lys Val Val Phe Ala Ala Asp Gly Ile Leu
 130 135 140
 Trp Pro Asp Lys Arg Leu Ala Asp Lys Tyr Pro Val Val His Ile Gly
 145 150 155 160
 Lys Arg Tyr Leu Asn Ser Gly Gly Phe Ile Gly Tyr Ala Pro Tyr Val
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 Asn Arg Ile Val Gln Gln Trp Asn Leu Gln Asp Asn Asp Asp Asp Gln
 180 185 190
 Leu Phe Tyr Thr Lys Val Tyr Ile Asp Pro Leu Lys Arg Glu Ala Ile
 195 200 205
 Asn Ile Thr Leu Asp His Lys Cys Lys Ile Phe Gln Thr Leu Asn Gly
 210 215 220
 Ala Val Asp Glu Val Val Leu Lys Phe Glu Asn Gly Lys Ala Arg Ala
 225 230 235 240
 Lys Asn Thr Phe Tyr Glu Thr Leu Pro Val Ala Ile Asn Gly Asn Gly
 245 250 255
 Pro Thr Lys Ile Leu Leu Asn Tyr Phe Gly Asn Tyr Val Pro Asn Ser
 260 265 270
 Trp Thr Gln Asp Asn Gly Cys Thr Leu Cys Glu Phe Asp Thr Val Asp
 275 280 285
 Leu Ser Ala Val Asp Val His Pro Asn Val Ser Ile Gly Val Phe Ile
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Glu Gln Pro Thr Pro Phe Leu Pro Arg Phe Leu Asp Ile Leu Leu Thr
 305 310 315 320
 Leu Asp Tyr Pro Lys Glu Ala Leu Lys Leu Phe Ile His Asn Lys Glu
 325 330 335
 Val Tyr His Glu Lys Asp Ile Lys Val Phe Phe Asp Lys Ala Lys His
 340 345 350
 Glu Ile Lys Thr Ile Lys Ile Val Gly Pro Glu Glu Asn Leu Ser Gln
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 Ala Glu Ala Arg Asn Met Gly Met Asp Phe Cys Arg Gln Asp Glu Lys
 370 375 380
 Cys Asp Tyr Tyr Phe Ser Val Asp Ala Asp Val Val Leu Thr Asn Pro
 385 390 395 400
 Arg Thr Leu Lys Ile Leu Ile Glu Gln Asn Arg Lys Ile Ile Ala Pro
 405 410 415
 Leu Val Thr Arg His Gly Lys Leu Trp Ser Asn Phe Trp Gly Ala Leu
 420 425 430
 Ser Pro Asp Gly Tyr Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val
 435 440 445
 Gln Gly Asn Arg Val Gly Val Trp Asn Val Pro Tyr Met Ala Asn Val
 450 455 460
 Tyr Leu Ile Lys Gly Lys Thr Leu Arg Ser Glu Met Asn Glu Arg Asn
 465 470 475 480
 Tyr Phe Val Arg Asp Lys Leu Asp Pro Asp Met Ala Leu Cys Arg Asn
 485 490 495
 Ala Arg Glu Met Thr Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu
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 Thr Phe Gln Met Leu Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser
 515 520 525
 Asn Arg His Glu Phe Gly Arg Leu Leu Ser Thr Ala Asn Tyr Asn Thr
 530 535 540
 Ser His Tyr Asn Asn Asp Leu Trp Gln Ile Phe Glu Asn Pro Val Asp
 545 550 555 560
 Trp Lys Glu Lys Tyr Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu
 565 570 575
 Asn Ile Val Glu Gln Pro Cys Pro Asp Val Phe Trp Phe Pro Ile Phe
 580 585 590
 Ser Glu Lys Ala Cys Asp Glu Leu Val Glu Glu Met Glu His Tyr Gly
 595 600 605

Lys Trp Ser Gly Gly Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr
 610 615 620
 Glu Asn Val Pro Thr Asp Asp Ile His Met Lys Gln Val Asp Leu Glu
 625 630 635 640
 Asn Val Trp Leu His Phe Ile Arg Glu Phe Ile Ala Pro Val Thr Leu
 645 650 655
 Lys Val Phe Ala Gly Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe
 660 665 670
 Val Val Lys Tyr Ser Pro Glu Arg Gln Arg Ser Leu Arg Pro His His
 675 680 685
 Asp Ala Ser Thr Phe Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu
 690 695 700
 Asp Phe Gln Gly Gly Gly Cys Lys Phe Leu Arg Tyr Asn Cys Ser Ile
 705 710 715 720
 Glu Ser Pro Arg Lys Gly Trp Ser Phe Met His Pro Gly Arg Leu Thr
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 His Leu His Glu Gly Leu Pro Val Lys Asn Gly Thr Arg Tyr Ile Ala
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<213> Homo sapiens

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 1 5 10 15

48

ctc cac ccc tgg aat ccc tgt ctg ggt gcg gac tcg gag aag ccc tcg
 Leu His Pro Trp Asn Pro Cys Leu Gly Ala Asp Ser Glu Lys Pro Ser
 20 25 30

96

agc atc ccc aca gat aaa tta tta gtc ata act gta gca aca aaa gaa	144
Ser Ile Pro Thr Asp Lys Leu Leu Val Ile Thr Val Ala Thr Lys Glu	
35 40 45	
agt gat gga ttc cat cga ttt atg cag tca gcc aaa tat ttc aat tat	192
Ser Asp Gly Phe His Arg Phe Met Gln Ser Ala Lys Tyr Phe Asn Tyr	
50 55 60	
act gtg aag gtc ctt ggt caa gga gaa gaa tgg aga ggt ggt gat gga	240
Thr Val Lys Val Leu Gly Gln Gly Glu Glu Trp Arg Gly Gly Asp Gly	
65 70 75 80	
att aat agt att gga ggg ggc cag aaa gtg aga tta atg aaa gaa gtc	288
Ile Asn Ser Ile Gly Gly Gly Gln Lys Val Arg Leu Met Lys Glu Val	
85 90 95	
atg gaa cac tat gct gat caa gat gat ctg gtt gtc atg ttt act gaa	336
Met Glu His Tyr Ala Asp Gln Asp Asp Leu Val Val Met Phe Thr Glu	
100 105 110	
tgc ttt gat gtc ata ttt gct ggt ggt cca gaa gaa gtt cta aaa aaa	384
Cys Phe Asp Val Ile Phe Ala Gly Gly Pro Glu Glu Val Leu Lys Lys	
115 120 125	
ttc caa aag gca aac cac aaa gtg gtc ttt gca gca gat gga att ttg	432
Phe Gln Lys Ala Asn His Lys Val Val Phe Ala Ala Asp Gly Ile Leu	
130 135 140	
tgg cca gat aaa aga cta gca gac aag tat cct gtt gtg cac att ggg	480
Trp Pro Asp Lys Arg Leu Ala Asp Lys Tyr Pro Val Val His Ile Gly	
145 150 155 160	
aaa cgc tat ctg aat tca gga gga ttt att ggc tat gct cca tat gtc	528
Lys Arg Tyr Leu Asn Ser Gly Gly Phe Ile Gly Tyr Ala Pro Tyr Val	
165 170 175	
aac cgt ata gtt caa caa tgg aat ctc cag gat aat gat gat gat cag	576
Asn Arg Ile Val Gln Gln Trp Asn Leu Gln Asp Asn Asp Asp Asp Gln	
180 185 190	
ctc ttt tac act aaa gtt tac att gat cca ctg aaa agg gaa gct att	624
Leu Phe Tyr Thr Lys Val Tyr Ile Asp Pro Leu Lys Arg Glu Ala Ile	
195 200 205	
aac atc aca ttg gat cac aaa tgc aaa att ttc cag acc tta aat gga	672
Asn Ile Thr Leu Asp His Lys Cys Lys Ile Phe Gln Thr Leu Asn Gly	
210 215 220	
gct gta gat gaa gtt gtt tta aaa ttt gaa aat ggc aaa gcc aga gct	720
Ala Val Asp Glu Val Val Leu Lys Phe Glu Asn Gly Lys Ala Arg Ala	
225 230 235 240	
aag aat aca ttt tat gaa aca tta cca gtg gca att aat gga aat gga	768
Lys Asn Thr Phe Tyr Glu Thr Leu Pro Val Ala Ile Asn Gly Asn Gly	
245 250 255	

ccc acc aag att ctc ctg aat tat ttt gga aac tat gta ccc aat tca	816
Pro Thr Lys Ile Leu Leu Asn Tyr Phe Gly Asn Tyr Val Pro Asn Ser	
260 265 270	
ttg aca cag gat aat ggc tgc act ctt tgt gaa ttc gat aca gtc gac	864
Trp Thr Gln Asp Asn Gly Cys Thr Leu Cys Glu Phe Asp Thr Val Asp	
275 280 285	
ttg tct gca gta gat gtc cat cca aac gta tca ata ggt gtt ttt att	912
Leu Ser Ala Val Asp Val His Pro Asn Val Ser Ile Gly Val Phe Ile	
290 295 300	
gag caa cca acc cct ttt cta cct cgg ttt ctg gac ata ttg ttg aca	960
Glu Gln Pro Thr Pro Phe Leu Pro Arg Phe Leu Asp Ile Leu Leu Thr	
305 310 315 320	
ctg gat tac cca aaa gaa gca ctt aaa ctt ttt att cat aac aaa gaa	1008
Leu Asp Tyr Pro Lys Glu Ala Leu Lys Leu Phe Ile His Asn Lys Glu	
325 330 335	
gtt tat cat gaa aag gac atc aag gta ttt ttt gat aaa gct aag cat	1056
Val Tyr His Glu Lys Asp Ile Lys Val Phe Phe Asp Lys Ala Lys His	
340 345 350	
gaa atc aaa act ata aaa ata gta gga cca gaa gaa aat cta agt caa	1104
Glu Ile Lys Thr Ile Lys Ile Val Gly Pro Glu Glu Asn Leu Ser Gln	
355 360 365	
gcg gaa gcc aga aac atg gga atg gac ttt tgc cgt cag gat gaa aag	1152
Ala Glu Ala Arg Asn Met Gly Met Asp Phe Cys Arg Gln Asp Glu Lys	
370 375 380	
tgt gat tat tac ttt agt gtg gat gca gat gtt gtt ttg aca aat cca	1200
Cys Asp Tyr Tyr Phe Ser Val Asp Ala Asp Val Val Leu Thr Asn Pro	
385 390 395 400	
agg act tta aaa att ttg att gaa caa aac aga aag atc att gct cct	1248
Arg Thr Leu Lys Ile Leu Ile Glu Gln Asn Arg Lys Ile Ile Ala Pro	
405 410 415	
ctt gta act cgt cat gga aag ctg tgg tcc aat ttc tgg gga gca ttg	1296
Leu Val Thr Arg His Gly Lys Leu Trp Ser Asn Phe Trp Gly Ala Leu	
420 425 430	
agt cct gat gga tac tat gca cga tct gaa gat tat gtg gat att gtt	1344
Ser Pro Asp Gly Tyr Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val	
435 440 445	
caa ggg aat aga gta gga gta tgg aat gtc cca tat atg gct aat gtg	1392
Gln Gly Asn Arg Val Gly Val Trp Asn Val Pro Tyr Met Ala Asn Val	
450 455 460	
tac tta att aaa gga aag aca ctc cga tca gag atg aat gaa agg aac	1440
Tyr Leu Ile Lys Gly Lys Thr Leu Arg Ser Glu Met Asn Glu Arg Asn	
465 470 475 480	

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Tyr Phe Val Arg Asp Lys Leu Asp Pro Asp Met Ala Leu Cys Arg Asn	
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Ala Arg Glu Met Thr Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu	
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Thr Phe Gln Met Leu Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser	
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Asn Arg His Glu Phe Gly Arg Leu Leu Ser Thr Ala Asn Tyr Asn Thr	
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tcc cat tat aac aat gac ctc tgg cag att ttt gaa aat cct gtg gac	1680
Ser His Tyr Asn Asn Asp Leu Trp Gln Ile Phe Glu Asn Pro Val Asp	
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Trp Lys Glu Lys Tyr Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu	
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Asn Ile Val Glu Gln Pro Cys Pro Asp Val Phe Trp Phe Pro Ile Phe	
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Ser Glu Lys Ala Cys Asp Glu Leu Val Glu Glu Met Glu His Tyr Gly	
595 600 605	
aaa tgg tct ggg gga aaa cat cat gat agc cgt ata tct ggt ggt tat	1872
Lys Trp Ser Gly Gly Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr	
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Glu Asn Val Pro Thr Asp Asp Ile His Met Lys Gln Val Asp Leu Glu	
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Asn Val Trp Leu His Phe Ile Arg Glu Phe Ile Ala Pro Val Thr Leu	
645 650 655	
aag gtc ttt gca ggc tat tat acg aag gga ttt gca cta ctg aat ttt	2016
Lys Val Phe Ala Gly Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe	
660 665 670	
gta gta aaa tac tcc cct gaa cga cag cgt tct ctt cgt cct cat cat	2064
Val Val Lys Tyr Ser Pro Glu Arg Gln Arg Ser Leu Arg Pro His His	
675 680 685	
gat gct tct aca ttt acc ata aac att gca ctt aat aac gtg gga gaa	2112
Asp Ala Ser Thr Phe Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu	
690 695 700	

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 Asp Phe Gln Gly Gly Gly Cys Lys Phe Leu Arg Tyr Asn Cys Ser Ile
 705 710 715 720

gag tca cca cga aaa ggc tgg agc ttc atg cat cct ggg aga ctc aca 2208
 Glu Ser Pro Arg Lys Gly Trp Ser Phe Met His Pro Gly Arg Leu Thr
 725 730 735

cat ttgcatgaag gacttcctgt taaaaatgga acaagataca ttgcagtgtc 2261
 His

atztatagat ccctaagtta tttacttttc attgaattga aatttatattt ggatgaatga 2321

ctggcatgaa cacgtctttg aagttgtggc tgagaagatg agaggaatat ttaaataaca 2381

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<212> PRT

<213> Homo sapiens

<400> 11

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Ser Ile Pro Thr Asp Lys Leu Leu Val Ile Thr Val Ala Thr Lys Glu
 35 40 45

Ser Asp Gly Phe His Arg Phe Met Gln Ser Ala Lys Tyr Phe Asn Tyr
 50 55 60

Thr Val Lys Val Leu Gly Gln Gly Glu Glu Trp Arg Gly Gly Asp Gly
 65 70 75 80

Ile Asn Ser Ile Gly Gly Gly Gln Lys Val Arg Leu Met Lys Glu Val
 85 90 95

Met Glu His Tyr Ala Asp Gln Asp Asp Leu Val Val Met Phe Thr Glu
 100 105 110

Cys Phe Asp Val Ile Phe Ala Gly Gly Pro Glu Glu Val Leu Lys Lys
 115 120 125

Phe	Gln	Lys	Ala	Asn	His	Lys	Val	Val	Phe	Ala	Ala	Asp	Gly	Ile	Leu	130	135	140	
Trp	Pro	Asp	Lys	Arg	Leu	Ala	Asp	Lys	Tyr	Pro	Val	Val	His	Ile	Gly	145	150	155	160
Lys	Arg	Tyr	Leu	Asn	Ser	Gly	Gly	Phe	Ile	Gly	Tyr	Ala	Pro	Tyr	Val	165	170	175	
Asn	Arg	Ile	Val	Gln	Gln	Trp	Asn	Leu	Gln	Asp	Asn	Asp	Asp	Asp	Gln	180	185	190	
Leu	Phe	Tyr	Thr	Lys	Val	Tyr	Ile	Asp	Pro	Leu	Lys	Arg	Glu	Ala	Ile	195	200	205	
Asn	Ile	Thr	Leu	Asp	His	Lys	Cys	Lys	Ile	Phe	Gln	Thr	Leu	Asn	Gly	210	215	220	
Ala	Val	Asp	Glu	Val	Val	Leu	Lys	Phe	Glu	Asn	Gly	Lys	Ala	Arg	Ala	225	230	235	240
Lys	Asn	Thr	Phe	Tyr	Glu	Thr	Leu	Pro	Val	Ala	Ile	Asn	Gly	Asn	Gly	245	250	255	
Pro	Thr	Lys	Ile	Leu	Leu	Asn	Tyr	Phe	Gly	Asn	Tyr	Val	Pro	Asn	Ser	260	265	270	
Trp	Thr	Gln	Asp	Asn	Gly	Cys	Thr	Leu	Cys	Glu	Phe	Asp	Thr	Val	Asp	275	280	285	
Leu	Ser	Ala	Val	Asp	Val	His	Pro	Asn	Val	Ser	Ile	Gly	Val	Phe	Ile	290	295	300	
Glu	Gln	Pro	Thr	Pro	Phe	Leu	Pro	Arg	Phe	Leu	Asp	Ile	Leu	Leu	Thr	305	310	315	320
Leu	Asp	Tyr	Pro	Lys	Glu	Ala	Leu	Lys	Leu	Phe	Ile	His	Asn	Lys	Glu	325	330	335	
Val	Tyr	His	Glu	Lys	Asp	Ile	Lys	Val	Phe	Phe	Asp	Lys	Ala	Lys	His	340	345	350	
Glu	Ile	Lys	Thr	Ile	Lys	Ile	Val	Gly	Pro	Glu	Glu	Asn	Leu	Ser	Gln	355	360	365	
Ala	Glu	Ala	Arg	Asn	Met	Gly	Met	Asp	Phe	Cys	Arg	Gln	Asp	Glu	Lys	370	375	380	
Cys	Asp	Tyr	Tyr	Phe	Ser	Val	Asp	Ala	Asp	Val	Val	Leu	Thr	Asn	Pro	385	390	395	400
Arg	Thr	Leu	Lys	Ile	Leu	Ile	Glu	Gln	Asn	Arg	Lys	Ile	Ile	Ala	Pro	405	410	415	
Leu	Val	Thr	Arg	His	Gly	Lys	Leu	Trp	Ser	Asn	Phe	Trp	Gly	Ala	Leu	420	425	430	

Ser Pro Asp Gly Tyr Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val
 435 440 445
 Gln Gly Asn Arg Val Gly Val Trp Asn Val Pro Tyr Met Ala Asn Val
 450 455 460
 Tyr Leu Ile Lys Gly Lys Thr Leu Arg Ser Glu Met Asn Glu Arg Asn
 465 470 475 480
 Tyr Phe Val Arg Asp Lys Leu Asp Pro Asp Met Ala Leu Cys Arg Asn
 485 490 495
 Ala Arg Glu Met Thr Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu
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 Thr Phe Gln Met Leu Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser
 515 520 525
 Asn Arg His Glu Phe Gly Arg Leu Leu Ser Thr Ala Asn Tyr Asn Thr
 530 535 540
 Ser His Tyr Asn Asn Asp Leu Trp Gln Ile Phe Glu Asn Pro Val Asp
 545 550 555 560
 Trp Lys Glu Lys Tyr Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu
 565 570 575
 Asn Ile Val Glu Gln Pro Cys Pro Asp Val Phe Trp Phe Pro Ile Phe
 580 585 590
 Ser Glu Lys Ala Cys Asp Glu Leu Val Glu Glu Met Glu His Tyr Gly
 595 600 605
 Lys Trp Ser Gly Gly Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr
 610 615 620
 Glu Asn Val Pro Thr Asp Asp Ile His Met Lys Gln Val Asp Leu Glu
 625 630 635 640
 Asn Val Trp Leu His Phe Ile Arg Glu Phe Ile Ala Pro Val Thr Leu
 645 650 655
 Lys Val Phe Ala Gly Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe
 660 665 670
 Val Val Lys Tyr Ser Pro Glu Arg Gln Arg Ser Leu Arg Pro His His
 675 680 685
 Asp Ala Ser Thr Phe Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu
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 Asp Phe Gln Gly Gly Gly Cys Lys Phe Leu Arg Tyr Asn Cys Ser Ile
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 Glu Ser Pro Arg Lys Gly Trp Ser Phe Met His Pro Gly Arg Leu Thr
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His

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<212> DNA

<213> Rattus rattus

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ctgccgtccc gggccccacg tctaaccgg tgctcttcgg ggtctccgcg tctcgcgaga 180

agtcctcgcc gcaggcctcg ggcttttcggg cttaggggcg g atg ggg gac cgc gga 236
Met Gly Asp Arg Gly
1 5

gtg agg ctg ggg ctg ctg atg ccc atg ctc gcc ctg ctc tcc tgg gcg 284
Val Arg Leu Gly Leu Leu Met Pro Met Leu Ala Leu Leu Ser Trp Ala
10 15 20

gct agc ctg ggc gta gcg gag gag act ccc tcg cgc atc cca gca gat 332
Ala Ser Leu Gly Val Ala Glu Glu Thr Pro Ser Arg Ile Pro Ala Asp
25 30 35

aag tta tta gtc ata act gta gca acc aaa gaa aac gat gga ttc cac 380
Lys Leu Leu Val Ile Thr Val Ala Thr Lys Glu Asn Asp Gly Phe His
40 45 50

aga ttt atg aat tca gcc aag tat ttc aat tat act gtg aag gtt ctt 428
Arg Phe Met Asn Ser Ala Lys Tyr Phe Asn Tyr Thr Val Lys Val Leu
55 60 65

ggg caa ggg caa gag tgg aga ggt ggt gat ggg atg aac agt att gga 476
Gly Gln Gly Gln Glu Trp Arg Gly Gly Asp Gly Met Asn Ser Ile Gly
70 75 80 85

ggg ggc cag aag gtg aga tta atg aaa gaa gcc atg gag cac tac gcc 524

Gly	Gln	Asp	Asp	Leu	Val	Ile	Leu	Phe	Thr	Glu	Cys	Phe	Asp	Val	Ile		
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ttt	gct	ggg	ggg	cct	gaa	gaa	ctt	ctt	aaa	aag	ttc	caa	aag	aca	aat	620	
Phe	Ala	Gly	Gly	Pro	Glu	Glu	Leu	Leu	Lys	Lys	Phe	Gln	Lys	Thr	Asn		
		120					125					130					
cat	aaa	atc	gtc	ttt	gca	gcg	gat	gcg	ctg	ttg	tgg	cca	gat	aag	cgg	668	
His	Lys	Ile	Val	Phe	Ala	Ala	Asp	Ala	Leu	Leu	Trp	Pro	Asp	Lys	Arg		
	135					140					145						
ctg	gca	gac	aag	tat	cct	ggg	gtg	cac	att	ggg	aaa	cgc	tac	ctg	aat	716	
Leu	Ala	Asp	Lys	Tyr	Pro	Gly	Val	His	Ile	Gly	Lys	Arg	Tyr	Leu	Asn		
150					155					160					165		
tct	gga	ggc	ttt	att	ggc	tat	gct	ccc	tac	atc	agc	cgt	ctg	gtc	cag	764	
Ser	Gly	Gly	Phe	Ile	Gly	Tyr	Ala	Pro	Tyr	Ile	Ser	Arg	Leu	Val	Gln		
				170					175					180			
cag	tgg	gat	ctg	cag	gat	aat	gat	gac	gac	cag	ctc	ttt	tac	act	aaa	812	
Gln	Trp	Asp	Leu	Gln	Asp	Asn	Asp	Asp	Asp	Gln	Leu	Phe	Tyr	Thr	Lys		
			185					190					195				
gtt	tac	atc	gac	ccg	ctg	aaa	agg	gaa	gct	ctt	aac	atc	aca	ttg	gat	860	
Val	Tyr	Ile	Asp	Pro	Leu	Lys	Arg	Glu	Ala	Leu	Asn	Ile	Thr	Leu	Asp		
		200					205					210					
cac	aga	tgc	aaa	att	ttc	cag	gcc	ttg	aat	gga	gct	aca	gac	gaa	gtt	908	
His	Arg	Cys	Lys	Ile	Phe	Gln	Ala	Leu	Asn	Gly	Ala	Thr	Asp	Glu	Val		
	215					220				225							
gtt	tta	aag	ttt	gaa	aat	ggg	aaa	agc	aga	gtg	aag	aat	aca	ttt	tat	956	
Val	Leu	Lys	Phe	Glu	Asn	Gly	Lys	Ser	Arg	Val	Lys	Asn	Thr	Phe	Tyr		
230				235						240					245		
gaa	aca	ctg	cca	gtg	gcc	atc	aat	ggg	aat	ggg	ccc	acc	aaa	att	ctc	1004	
Glu	Thr	Leu	Pro	Val	Ala	Ile	Asn	Gly	Asn	Gly	Pro	Thr	Lys	Ile	Leu		
				250				255						260			
ttg	aat	tac	ttt	gga	aac	tat	gtt	cca	aat	tca	tgg	aca	cag	gaa	aat	1052	
Leu	Asn	Tyr	Phe	Gly	Asn	Tyr	Val	Pro	Asn	Ser	Trp	Thr	Gln	Glu	Asn		
			265				270						275				
ggc	tgt	gct	ctt	tgt	gac	ttt	gac	aca	att	gac	ctg	tct	aca	gta	gat	1100	
Gly	Cys	Ala	Leu	Cys	Asp	Phe	Asp	Thr	Ile	Asp	Leu	Ser	Thr	Val	Asp		
		280					285					290					
gtc	tat	ccg	aag	gta	aca	cta	ggg	gtt	ttt	att	gaa	caa	cca	acc	ccc	1148	
Val	Tyr	Pro	Lys	Val	Thr	Leu	Gly	Val	Phe	Ile	Glu	Gln	Pro	Thr	Pro		
		295				300					305						
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Phe	Leu	Pro	Arg	Phe	Leu	Asp	Leu	Leu	Leu	Thr	Leu	Asp	Tyr	Pro	Lys		
310					315					320					325		
gaa	gca	ctt	cga	ctc	ttt	gtc	cat	aat	aaa	gaa	gtt	tat	cat	gaa	aag	1244	
Glu	Ala	Leu	Arg	Leu	Phe	Val	His	Asn	Lys	Glu	Val	Tyr	His	Glu	Lys		
				330					335					340			

gac atc aaa gcg ttt gtt gat aaa gct aaa cac gac atc agc tct ata	1292
Asp Ile Lys Ala Phe Val Asp Lys Ala Lys His Asp Ile Ser Ser Ile	
345 350 355	
aaa ata gta gga cca gag gaa aat cta agt caa gcg gaa gcc aga aac	1340
Lys Ile Val Gly Pro Glu Glu Asn Leu Ser Gln Ala Glu Ala Arg Asn	
360 365 370	
atg gga atg gat ttc tgc cgt cag gat gaa aag tgt gat tac tac ttt	1388
Met Gly Met Asp Phe Cys Arg Gln Asp Glu Lys Cys Asp Tyr Tyr Phe	
375 380 385	
agt gtg gat gca gat gtt gtt ttg aca aac cca aga act tta aaa att	1436
Ser Val Asp Ala Asp Val Val Leu Thr Asn Pro Arg Thr Leu Lys Ile	
390 395 400 405	
ttg att gaa caa aac agg aag atc att gcc cct ctt gtg aca cgt cat	1484
Leu Ile Glu Gln Asn Arg Lys Ile Ile Ala Pro Leu Val Thr Arg His	
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gga aag ttg tgg tcc aac ttc tgg gga gcc ctg agt cct gat gga tac	1532
Gly Lys Leu Trp Ser Asn Phe Trp Gly Ala Leu Ser Pro Asp Gly Tyr	
425 430 435	
tat gct cgt tct gaa gat tac gta gat atc gtt cag gga aac aga gta	1580
Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val Gln Gly Asn Arg Val	
440 445 450	
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Gly Ile Trp Asn Val Pro Tyr Met Ala Asn Val Tyr Leu Ile Gln Gly	
455 460 465	
aag acg ctg cga tca gag atg agt gaa agg aac tat ttt gtg cgt gat	1676
Lys Thr Leu Arg Ser Glu Met Ser Glu Arg Asn Tyr Phe Val Arg Asp	
470 475 480 485	
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Lys Leu Asp Pro Asp Met Ser Leu Cys Arg Asn Ala Arg Asp Met Thr	
490 495 500	
tta caa agg gaa aaa gac tcc ccc act ccg gaa aca ttc caa atg ctc	1772
Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu Thr Phe Gln Met Leu	
505 510 515	
agc ccc cca aag ggt gtg ttt atg tac att tct aac aga cat gaa ttt	1820
Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser Asn Arg His Glu Phe	
520 525 530	
gga cgg ctg ata tca act gct aat tac aac act tcc cat ctc aac aat	1868
Gly Arg Leu Ile Ser Thr Ala Asn Tyr Asn Thr Ser His Leu Asn Asn	
535 540 545	
gac ctc tgg cag atc ttt gaa aat ccc gtg gat tgg aag gaa aaa tat	1916
Asp Leu Trp Gln Ile Phe Glu Asn Pro Val Asp Trp Lys Glu Lys Tyr	
550 555 560 565	

ata aac cgt gac tat tca aag att ttc act gaa aat ata gtc gag cag	1964
Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu Asn Ile Val Glu Gln	
570 575 580	
ccc tgt cca gat gtc ttc tgg ttt ccc ata ttt tct gaa cga gcc tgt	2012
Pro Cys Pro Asp Val Phe Trp Phe Pro Ile Phe Ser Glu Arg Ala Cys	
585 590 595	
gac gag ttg gta gaa gaa atg gaa cat tac ggc aag tgg tcc ggg gga	2060
Asp Glu Leu Val Glu Glu Met Glu His Tyr Gly Lys Trp Ser Gly Gly	
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aag cat cat gac agc cgt ata tct ggt ggc tat gaa aat gtc cca acg	2108
Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr Glu Asn Val Pro Thr	
615 620 625	
gat gac att cat atg aag cag att gac ctg gag aac gtc tgg ctt cac	2156
Asp Asp Ile His Met Lys Gln Ile Asp Leu Glu Asn Val Trp Leu His	
630 635 640 645	
ttt atc cga gag ttt atc gct cca gtt acc ctg aag gtc ttc gcg gga	2204
Phe Ile Arg Glu Phe Ile Ala Pro Val Thr Leu Lys Val Phe Ala Gly	
650 655 660	
tat tac acc aag gga ttt gcc ctg ctg aac ttc gta gtg aag tac tcg	2252
Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe Val Val Lys Tyr Ser	
665 670 675	
ccc gaa aga cag cgc tcg ctc cgg cct cac cac gat gcg tca acc ttc	2300
Pro Glu Arg Gln Arg Ser Leu Arg Pro His His Asp Ala Ser Thr Phe	
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acc atc aac att gct cta aat aat gta gga gag gat ttt cag gga ggt	2348
Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu Asp Phe Gln Gly Gly	
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gga tgc aaa ttc cta agg tat aat tgc tcc atc gaa tcc ccc cga aaa	2396
Gly Cys Lys Phe Leu Arg Tyr Asn Cys Ser Ile Glu Ser Pro Arg Lys	
710 715 720 725	
ggc tgg agc ttc atg cat cct ggg agg ctt act cat cta cac gaa ggg	2444
Gly Trp Ser Phe Met His Pro Gly Arg Leu Thr His Leu His Glu Gly	
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ctt cct gtc aaa aat gga aca aga tac att gca gtc tca ttt	2486
Leu Pro Val Lys Asn Gly Thr Arg Tyr Ile Ala Val Ser Phe	
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<210> 13

<211> 755

<212> PRT

<213> Rattus rattus

<400> 13

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		20						25					30		
Arg	Ile	Pro	Ala	Asp	Lys	Leu	Leu	Val	Ile	Thr	Val	Ala	Thr	Lys	Glu
		35						40					45		
Asn	Asp	Gly	Phe	His	Arg	Phe	Met	Asn	Ser	Ala	Lys	Tyr	Phe	Asn	Tyr
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Thr Val Lys Val Leu Gly Gln Gly Gln Glu Trp Arg Gly Gly Asp Gly
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 Met Asn Ser Ile Gly Gly Gly Gln Lys Val Arg Leu Met Lys Glu Ala
 85 90 95
 Met Glu His Tyr Ala Gly Gln Asp Asp Leu Val Ile Leu Phe Thr Glu
 100 105 110
 Cys Phe Asp Val Ile Phe Ala Gly Gly Pro Glu Glu Leu Leu Lys Lys
 115 120 125
 Phe Gln Lys Thr Asn His Lys Ile Val Phe Ala Ala Asp Ala Leu Leu
 130 135 140
 Trp Pro Asp Lys Arg Leu Ala Asp Lys Tyr Pro Gly Val His Ile Gly
 145 150 155 160
 Lys Arg Tyr Leu Asn Ser Gly Gly Phe Ile Gly Tyr Ala Pro Tyr Ile
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 Ser Arg Leu Val Gln Gln Trp Asp Leu Gln Asp Asn Asp Asp Asp Gln
 180 185 190
 Leu Phe Tyr Thr Lys Val Tyr Ile Asp Pro Leu Lys Arg Glu Ala Leu
 195 200 205
 Asn Ile Thr Leu Asp His Arg Cys Lys Ile Phe Gln Ala Leu Asn Gly
 210 215 220
 Ala Thr Asp Glu Val Val Leu Lys Phe Glu Asn Gly Lys Ser Arg Val
 225 230 235 240
 Lys Asn Thr Phe Tyr Glu Thr Leu Pro Val Ala Ile Asn Gly Asn Gly
 245 250 255
 Pro Thr Lys Ile Leu Leu Asn Tyr Phe Gly Asn Tyr Val Pro Asn Ser
 260 265 270
 Trp Thr Gln Glu Asn Gly Cys Ala Leu Cys Asp Phe Asp Thr Ile Asp
 275 280 285
 Leu Ser Thr Val Asp Val Tyr Pro Lys Val Thr Leu Gly Val Phe Ile
 290 295 300
 Glu Gln Pro Thr Pro Phe Leu Pro Arg Phe Leu Asp Leu Leu Leu Thr
 305 310 315 320
 Leu Asp Tyr Pro Lys Glu Ala Leu Arg Leu Phe Val His Asn Lys Glu
 325 330 335
 Val Tyr His Glu Lys Asp Ile Lys Ala Phe Val Asp Lys Ala Lys His
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 Asp Ile Ser Ser Ile Lys Ile Val Gly Pro Glu Glu Asn Leu Ser Gln
 355 360 365

Ala Glu Ala Arg Asn Met Gly Met Asp Phe Cys Arg Gln Asp Glu Lys
 370 375 380
 Cys Asp Tyr Tyr Phe Ser Val Asp Ala Asp Val Val Leu Thr Asn Pro
 385 390 395 400
 Arg Thr Leu Lys Ile Leu Ile Glu Gln Asn Arg Lys Ile Ile Ala Pro
 405 410 415
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 Ser Pro Asp Gly Tyr Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val
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 Gln Gly Asn Arg Val Gly Ile Trp Asn Val Pro Tyr Met Ala Asn Val
 450 455 460
 Tyr Leu Ile Gln Gly Lys Thr Leu Arg Ser Glu Met Ser Glu Arg Asn
 465 470 475 480
 Tyr Phe Val Arg Asp Lys Leu Asp Pro Asp Met Ser Leu Cys Arg Asn
 485 490 495
 Ala Arg Asp Met Thr Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu
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 Thr Phe Gln Met Leu Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser
 515 520 525
 Asn Arg His Glu Phe Gly Arg Leu Ile Ser Thr Ala Asn Tyr Asn Thr
 530 535 540
 Ser His Leu Asn Asn Asp Leu Trp Gln Ile Phe Glu Asn Pro Val Asp
 545 550 555 560
 Trp Lys Glu Lys Tyr Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu
 565 570 575
 Asn Ile Val Glu Gln Pro Cys Pro Asp Val Phe Trp Phe Pro Ile Phe
 580 585 590
 Ser Glu Arg Ala Cys Asp Glu Leu Val Glu Glu Met Glu His Tyr Gly
 595 600 605
 Lys Trp Ser Gly Gly Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr
 610 615 620
 Glu Asn Val Pro Thr Asp Asp Ile His Met Lys Gln Ile Asp Leu Glu
 625 630 635 640
 Asn Val Trp Leu His Phe Ile Arg Glu Phe Ile Ala Pro Val Thr Leu
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 Lys Val Phe Ala Gly Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe
 660 665 670

Val Val Lys Tyr Ser Pro Glu Arg Gln Arg Ser Leu Arg Pro His His
675 680 685

Asp Ala Ser Thr Phe Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu
690 695 700

Asp Phe Gln Gly Gly Gly Cys Lys Phe Leu Arg Tyr Asn Cys Ser Ile
705 710 715 720

Glu Ser Pro Arg Lys Gly Trp Ser Phe Met His Pro Gly Arg Leu Thr
725 730 735

His Leu His Glu Gly Leu Pro Val Lys Asn Gly Thr Arg Tyr Ile Ala
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Val Ser Phe
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<210> 14

<211> 1486

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(396)

<400> 14

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His Gly Glu Gly Gly Gly Glu Glu Ala Ala Ala Ala Arg Glu Arg	
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gga tcg gcg tcc ggg gaa ccc ccg tct ggc tcc ggc cgc ggc aag aag	144
Gly Ser Ala Ser Gly Glu Pro Pro Ser Gly Ser Gly Arg Gly Lys Lys	
35 40 45	
atc ttc ggc tgc tcc gag tgc gag aag ctg ttc cgc tca ccg cga gac	192
Ile Phe Gly Cys Ser Glu Cys Glu Lys Leu Phe Arg Ser Pro Arg Asp	
50 55 60	
ctg gag cgg cac gtg ctg gtg cac act ggc gag aag ccg ttc ccg tgc	240
Leu Glu Arg His Val Leu Val His Thr Gly Glu Lys Pro Phe Pro Cys	

65	70	75	80	
ctg gag tgc ggc aag ttc ttc cgc cac gag tgc tac ctc aag cgc cac				288
Leu Glu Cys Gly Lys Phe Phe Arg His Glu Cys Tyr Leu Lys Arg His				
	85	90	95	
cga ctg ctg cac ggc acc gag cgg ccc ttc cct tgc cac atc tgc ggc				336
Arg Leu Leu His Gly Thr Glu Arg Pro Phe Pro Cys His Ile Cys Gly				
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Lys Gly Phe Ile Thr Leu Ser Asn Leu Ser Arg His Leu Lys Leu His				
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Arg Gly Met Asp				
130				
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<210> 15
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 15

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Gly	Ser	Ala	Ser	Gly	Glu	Pro	Pro	Ser	Gly	Ser	Gly	Arg	Gly	Lys	Lys
		35						40				45			
Ile	Phe	Gly	Cys	Ser	Glu	Cys	Glu	Lys	Leu	Phe	Arg	Ser	Pro	Arg	Asp
	50					55				60					
Leu	Glu	Arg	His	Val	Leu	Val	His	Thr	Gly	Glu	Lys	Pro	Phe	Pro	Cys
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Leu	Glu	Cys	Gly	Lys	Phe	Phe	Arg	His	Glu	Cys	Tyr	Leu	Lys	Arg	His
			85					90						95	
Arg	Leu	Leu	His	Gly	Thr	Glu	Arg	Pro	Phe	Pro	Cys	His	Ile	Cys	Gly
			100					105					110		
Lys	Gly	Phe	Ile	Thr	Leu	Ser	Asn	Leu	Ser	Arg	His	Leu	Lys	Leu	His
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Arg	Gly	Met	Asp												
		130													

<210> 16
 <211> 580
 <212> DNA
 <213> Homo sapiens

<400> 16

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<210> 17

<211> 120

<212> PRT

<213> Homo sapiens

<400> 17

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			20					25					30		
Phe	His	Arg	Gln	Phe	Leu	Leu	Gln	Gly	Arg	Leu	Asn	Gln	Ala	Lys	Ile
		35					40					45			
Asn	Thr	His	Trp	Tyr	Thr	Trp	Leu	Pro	Thr	Asn	Phe	Ile	Cys	Ile	Tyr
		50				55					60				
Ile	Phe	Tyr	Phe	Gln	His	Pro	His	Ser	Ser	Trp	Phe	Asn	Gln	Ser	Leu
65					70					75				80	
Val	Leu	Ala	Asn	Asn	Lys	Leu	Val	Arg	Arg	Ser	Lys	Val	Val	Asp	Val
			85						90					95	
Cys	Thr	Trp	Leu	Pro	Trp	Arg	Ser	Ser	Gly	Asp	Ser	Leu	Phe	Gln	Asn
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<210> 18

<211> 4342

<212> DNA

<213> Homo sapiens

<400> 18

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<210> 21

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35 40 45
Pro Ser Asp Gly Leu Ser Asn Thr Glu Ser Ser Asp Gly Leu Asn Lys
50 55 60
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65 70 75 80
Val Arg Glu Lys Ser Glu Phe Ile Leu Lys Ser Ile Gln Glu Leu Gly
85 90 95
Ile Arg Ile Pro Arg Pro Leu Gly Gln Gly Pro Ser Arg Phe Ile Pro
100 105 110
Glu Lys Glu Ile Leu Gln Val Gly Ser Glu Asp Ala Gln Met His Ala
115 120 125
Leu Phe Ala Asp Ser Phe Ala Ala Leu Gly Arg Leu Asp Asn Ile Thr
130 135 140
Leu Val Met Val Phe His Pro Gln Tyr Leu Glu Ser Phe Leu Lys Thr
145 150 155 160
Gln His Tyr Leu Leu Gln Met Asp Gly Pro Leu Pro Leu His Tyr Arg
165 170 175
His Tyr Ile Gly Ile Met Ala Ala Ala Arg His Gln Cys Ser Tyr Leu
180 185 190
Val Asn Leu His Val Asn Asp Phe Leu His Val Gly Gly Asp Pro Lys
195 200 205
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210 215 220
Glu Leu Asn Lys Val Leu Ala His Arg Pro Trp Leu Ile Thr Lys Glu
225 230 235 240
His Ile Glu Gly Leu Leu Lys Ala Glu Glu His Ser Trp Ser Leu Ala
245 250 255
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275 280 285

Gly His Thr Phe Arg Pro Pro Ser Val Ser Asn Tyr Cys Ile Cys Asp
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 Ile Thr Asn Gly Asn His Ser Val Asp Glu Met Pro Val Asn Ser Ala
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 325 330 335
 Glu Lys Met Arg Gln Leu Gln Glu Cys Arg Asp Glu Glu Glu Ala Ser
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 Gln Glu Glu Met Ala Ser Arg Phe Glu Ile Glu Lys Arg Glu Ser Met
 355 360 365
 Phe Val Phe Ser Ser Asp Asp Glu Glu Val Thr Pro Ala Arg Ala Val
 370 375 380
 Ser Arg His Phe Glu Asp Thr Ser Tyr Gly Tyr Lys Asp Phe Ser Arg
 385 390 395 400
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 Asp His Gly Tyr Ser Leu Val Asn Arg Leu Tyr Pro Asp Val Gly Gln
 420 425 430
 Leu Ile Asp Glu Lys Phe His Ile Ala Tyr Asn Leu Thr Tyr Asn Thr
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 Met Ala Met His Lys Asp Val Asp Thr Ser Met Leu Arg Arg Ala Ile
 450 455 460
 Trp Asn Tyr Ile His Cys Met Phe Gly Ile Arg Tyr Asp Asp Tyr Asp
 465 470 475 480
 Tyr Gly Glu Ile Asn Gln Leu Leu Asp Arg Ser Phe Lys Val Tyr Ile
 485 490 495
 Lys Thr Val Val Cys Thr Pro Glu Lys Val Thr Lys Arg Met Tyr Asp
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 Ser Phe Trp Arg Gln Phe Lys His Ser Glu Lys Val His Val Asn Leu
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 Ala Ile Thr Arg Tyr Met Thr
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